CLAIMS:

1. A family A DNA polymerase which has a modified motif C sequence and an enhanced mismatch discrimination as compared to the corresponding wild type polymerase, or a Klenow fragment thereof, wherein in the motif C sequence QVH in positions 879-881, based on the *E. coli* DNA polymerase Klenow fragment shown in SEQ ID NO: 2, at least the amino acid residue Q879 has been replaced by a lipophilic amino acid residue.

2. The DNA polymerase or its Klenow fragment according to claim 1, which is a bacterial DNA polymerase, preferably a thermostable DNA polymerase, more preferably selected from the group consisting of polymerases from *Thermus thermophilus, Thermus filiformis, Rhodothermus obamensis* or *Bacillus stearothermophilus*.

3. The DNA polymerase or its Klenow fragment according to claim 1 or 2, wherein in the motif C sequence QVH in positions 879-881:

   (i) H881 has been further replaced by a lipophilic amino acid residue; and/or

   (ii) the amino acid residue in position 880 is Val, Leu, Ile, Ala or Tyr, especially Val or Ile.

4. The DNA polymerase or its Klenow fragment according to one or more of claims 1 to 3, wherein said lipophilic amino acid residue is selected from Gly, Ala, Val, Leu, Ile, Pro, Phe, Met and Trp, preferably from Gly, Ala, Val, Leu and Ile, and more preferably the motif C sequence QVH has been replaced by the sequence LVL or LVG.

5. The DNA polymerase or its Klenow fragment according to one or more of claims 1 to 4:

   (i) which is a Taq polymerase with the sequence shown in SEQ ID NO: 4 in which the sequence QVH in positions 782-784 has been replaced by LVL or LVG; or

   (ii) which is a Klenow fragment with the sequence shown in SEQ ID NO: 2 in which the sequence QVH in positions 879-881 has been replaced by LVL or LVG.

6. A DNA sequence which codes for a DNA polymerase or its Klenow fragment according to one or more of claims 1 to 5.

7. A vector which contains the DNA sequence according to claim 6.

8. A host cell which has been transformed with the vector according to claim 7 and/or includes a DNA according to claim 6.

9. A process for the preparation of a DNA polymerase or its Klenow fragment according to one or more of claims 1 to 5, which comprises culturing a host cell according to claim 8 and isolating the DNA polymerase or the Klenow fragment from the culture or the culture supernatant.

10. Use of the DNA polymerase or the Klenow fragment according to one or more of claims 1 to 5 in diagnostic and molecular-biological methods including allele-specific PCR, DNA amplification by means of PCR, cloning, etc.

11. A method for determining the presence or absence of at least one sequence variant in one or more target nucleic acids in an individual sample, which comprises using a DNA polymerase according to one or more of claims 1 to 5.

12. The method according to claim 11 including the following steps:

a) adding:

- deoxynucleoside triphosphates;
- a DNA polymerase according to one or more of claims 1 to 5;
- at least one discriminating primer containing at least one discriminating nucleotide residue, wherein a primer is added for each sequence variant to be detected of a target nucleic acid, which primer has a sequence complementary to the sequence variant to be detected, and wherein the sequence variant to be detected in the target nucleic acid is complementary to at least one 3'-terminal, 3'-proxi-terminal or 3'-proxi-proxi-terminal nucleotide residue of the discriminating primer;
- at least one other primer which is complementary to a primer extension product formed by extension of a discriminating primer;

b) performing a primer extension reaction wherein an extension product of the discriminating primer is obtained substantially only if the sample contains a target nucleic acid with the sequence variant to be detected;

c) separating the product of the primer extension reaction from the template nucleic acid;

d) reiterating steps b) and c) to obtain an amplification product, for example, by polymerase chain reaction; and

e) determining the presence or absence of a sequence variant from the presence or absence of the amplification product.

13. The method according to claim 12, wherein steps b) to e) are performed as real-time PCR or real-time RT-PCR.

14. A kit for determining the presence or absence of at least one sequence variant in one or more target nucleic acids in an individual sample according to claims 11 to 13, containing at least one DNA polymerase according to claims 1 to 5.

15. The kit according to claim 14, additionally containing one or more of the following components:

- one or more discriminating primers containing at least one discriminating nucleotide residue, wherein the sequence variant to be detected in the target nucleic acid is complementary to at least one 3'-terminal, 3'-proxi-terminal or 3'-proxi-proxi-terminal nucleotide residue of the discriminating primer;

- one or more other primers which are complementary to a primer extension product formed by extension of said discriminating primers;

- deoxynucleoside triphosphates;

- buffers;

- quantification reagents, especially intercalating reagents or reagents binding to the minor groove; and

- polymerase-blocking antibodies, especially TaqBlock.